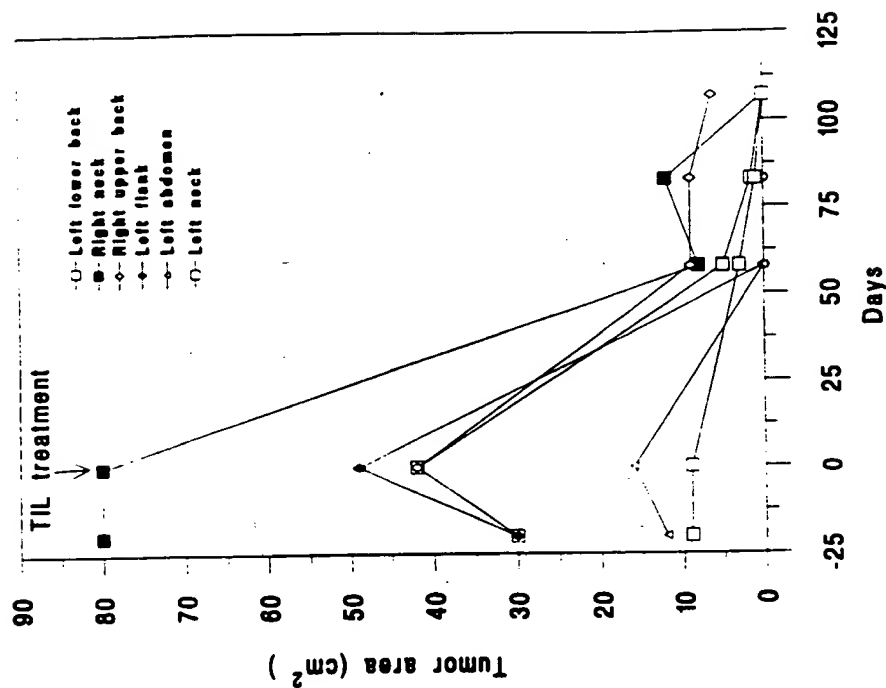


FIGURE 2

FIGURE 3A



FIGURE 3B



GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCT	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTTGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGAAGT	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCCTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

FIGURE 4

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACCTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTGGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIGURE 4 (continued)

FIGURE 5A

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1 MDLVLKRCLL HLAIVIGALLA VGATKVPRNQ DWLGVSQRQLR TKAWNROQLYP
51 EWTEAQRLLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPDG
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSTGY
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVPGTT DGHRTAEAP NNTAGQVPTT EVVGTTPGQA PTAEPSTGTS
351 VQVPTTEVIS TAPVQMPAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGSLGPLLLDG TATLRLVKRO VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STOLIMPGQE AGLQVPLIV
601 GILLVLMVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

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FIGURE 5B

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Pme117 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----
gp100 M-----V-----Q-----L-----
cDNA25FL M-----F-----Q-----L-----
cDNA25TR Q-----L-----PPQWAAGLSTLI
1 162 236 274 588 649

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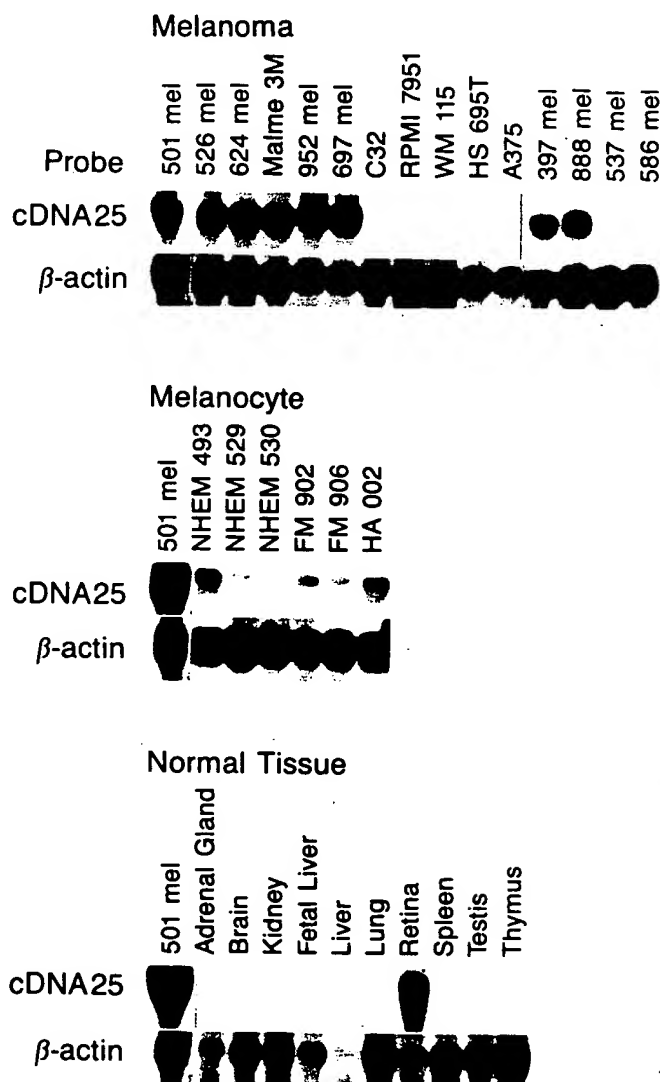


FIGURE 6

FIGURE 7A

1 MDLVLRCLL HLAIVIGALLA VGATKVPRNQ DWLGVSRLR TKAWNRLYP
D3-----
D5-----
D4-----
C4-----
51 EWTEAQLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
D3-----
D5-----
D4-----
C4-----
101 QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
D3-----
D5-----
D4-----
C4-----
151 YVWKTWGOYW QVLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
D3----D3
D5----- --D5
D4-----
C4-----
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSPGY
C4-----
25TR-----
251 LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
C4-----C4
25TR-----
301 CGSSPVP GTT DGHRTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSTTS
25TR-----
351 VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
25TR-----
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
25TR-----
451 TGS LGP LLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
25TR-----
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCQPPAQL CQVLPSPAC
25TR-----
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
25TR-----
601 GILLVLMVAV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
25TR-----
651 ENSPLLSGQQ V
25TR----- -25TR

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FIGURE 7B

DNA fragment	620-1	620-2	TIL 660-1	1143	1200
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D3	-	-	-	-	-
D5	-	+	-	-	+
D4	-	+	-	-	+
C4	+	+	+	+	+
25TR	-	-	+	+	+

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